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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 6, 2005, 06:11:39 ; Search time 93 Seconds (without alignments) 897.515 Million cell updates/sec

Title: US-10-616-410-2
Perfect score: 952
Sequence: 1 MADEEKLPPGWEKRMSRSSG......GENSGPVFTDSGIHIILRTE 163

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

							-																										
		Description	Q13526 homo sapien		Q9i9k6 xenopus lae	Q642n3 xenopus tro		Q6azr5 xenopus lae				Q9n492 caenorhabdi	07rvy7 neurospora	O60045 neurospora	Q6uay2 paracoccidi		074448 schizosacch		Q6cmz3 kluyveromyc	Q9c475 candida alb	Q8njn5 cryptococcu	_				Q75cn9 ashbya goss				Q94g00 malus domes	Q9lek8 digitalis l	Q7xtk0 oryza sativ	Q8irj5 drosophila
		:																٠															
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SUMMARIES		TI OI	PIN1 HUMAN	PIN1 MOUSE	Q919 <u>K</u> 6	Q642N3	Q6DEB1	Q6AZR5	Q6PBX1	Q7QAB6	DOD DROME	Q9N492	Q7RVY7	SSP1_NEUCR	Q6UAY2	042735	PIN1 SCHPO	Q6CEL8	Q6CMZ3	Q9C475	Q8NJN5	Q6BRV8	ESS1_YEAST	Q6FXP9	P90527	075CN9	Q7QAB7	PINI ARATH		PIN1_MALDO	PINI_DIGLA	Q7XTK0	QBIRJS
		DB	-	-	~	~	N	7	~	~	н	~	~	-	0	7	-	~	~	0	~	7	-	0	~	0	7	-		-	Н	7	0
		Length	163	165	159	159	159	158	159	191	166	168	186	182	190	176	175	185	162	177	178	177	190	173	243	163	148	119	100	121	118	123	386
		Match	100.0	95.5	88.4	88.3	88.1	87.8	79.9	57.6	53.6	51.2	50.9	50.3	47.9	46.6	45.6	45.4	43.4	43.4	42.7	42.3	41.8	41.3	41.3	40.0	39.7	35.3	34.9	34.8	33.2	32.9	32.5
		Score	852	814	753	752	751	748	681	491	456.5	436	433.5	428.5	408.5	397	388.5	387	370	369.5	364	360	356.5	352	351.5	341	338	301	297	296.5	283	280	277
	1000	No.	7	8	m	4	2	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	22	56	27	28	53	30	31

QBBrs5 encephalito Q6mr41 bdellovibr1 Q7264 deaulfovibr Q82su8 nitrosomona Q74bg7 geobacter Q89994 clostridium P24327 becillus su O74049 cenarchaeum Q74ae7 geobacter s Q6esk5 oryza sativ Q6esk5 oryza sativ Q6514 bartonella Q6514 bartonella
08SRS5 06MR41 022D64 082SD8 074BG7 0895G4 PRSA BACSU 074049 077AB9 077AB9 071AB9 076ESK5 06GSU1 06GSU1
000000H0000000
150 629 630 3321 246 246 247 247 317 317
25.00 20.00
218.5 186.5 186 185 181 180.5 177 176 176 176 176 178.5
wwwwwwwaaaaaa awaww

ALIGNMENTS

RESULT 1

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                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
activity. Displays a preference for an acidic residue N-terminal to the isomerized proline bond. Catalyzing pSer/Thr-Pro cis/trans
                                CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00456; WW; 1.
PROSITE; PS01096; PPIC PPIASE 1; 1.
PROSITE; PS01199; PPIC PPIASE 2; 1.
PROSITE; PS01159; WW DOMAIN 1; 1.
PROSITE; PS50020; WW DOMAIN 2; 1.
3D-structure; Cell cycle; ISomerase; Nuclear protein; Rotamase.
                                                            -!- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 852; DB 1; Length 163; 100.0%; Pred. No. 3e-70; ive 0; Mismatches 0; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18243 MW; 35391AF40B7D1E13 CRC64;
                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                            (omega=0).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                     EMBL; U49070; AAC50492.1; -.
EMBL; BC002899; AAH02899.1; -
PIR; S68520; S68520.
                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00639; Rotamase; 1.
Pfam; PF00397; WW; 1.
                                                                                                                                                                                                                       1F8A; X-ray; B=1-163.
                                                                                                                                                                                                                                                                                       1PIN; X-ray; A=1-163
                                                                                                                                                                                                                                 116C; NMR; A=6-44.
118G; NMR; B=6-44.
118H; NMR; B=6-44.
                                                                                                                                                                                                                                                                                               Genew, HGNC:8988; PIN1.
H-InvDB, HIX0014730; -.
MIM; 601052; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAND
STRAND
SEQUENCE
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STRAND
TURN
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HBLIX
HBLIX
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Gaps

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Conservative

Similarity

Best Local Sim Matches 163;

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RECURENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=C57BL/6J; TISSUE=Embryo, and Kidney;

MININE_C57BL/6J; TISSUE=Embryo, and Kidney;

MININE_C57BL/6J; TISSUE=Embryo, and Kidney;

RA MININE STRAIN=C57BL/6J; TISSUE=Embryo, and Kidney;

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Balas Y., Hill D.P., Bulf C., Hume D.A., Canonbach C., Gojobori T.,

RA Balas J.A., Bradel D., Brusic V., Chothia C., Corbinson, S.,

RA Balas G., M., Bradel D., Brusic V., Chothia C., Corbinson, Frazer K.S.,

RA Balas G., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedairski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedairski R.M., King B.L.,

RA Majlott D.K., Maltais L., Marchionni L., Morkenzie L., Mikh H.,

RA Nagashhma T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,

Sultana R., Takenaka Y., Taylor B.S., Teasdale R.D., Tomita M.,

RA Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,

Milming L.G., Wynnew Boris A., Vanagisawa M., Yang I.,

Wilming L.G., Wynnew Boris A., Vanagisawa M., Yang I.,

Hivozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Alzawa K., Shimagawa T., Pukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishiata K., Shinagawa B.,

Maninaki A., Sakai K., Sasaki D., Shibata R., Silopara J.,

RA Wasani H., Sakai K., Sasaki D., Shibata R., Silopara J.,

Ra Mara A., Hashizume W., Imotani K., Ishiata R., Silopara J.,

Manining M. Sarai K., Sasaki D., Shibata R., Shinagawa R.,

Ra Mara A., Hashizume W., Imotani K., Ishiat Y., Itoh M., Kagawa I.,

Ra Manining R. Sandali M., Saraki D., Shibata R., Shinagawa R.,

Ra Manining R., Sandali M., Saraki D., Shibata R., Shinaya M.,

Ra Manining R., Sandali M., Saraki D., Shibata R., Shinaya M.,

Ra Manining
                                                                                                                                                    61 LVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDPRSLASQPSDCSSAKARG 120
                                                                                                             LVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKARG 120
                           1 MADERICL PPGWEKRANSRSGRVYYFWHITINASQWERPSGNSSSGGKNGGGEPARVRCSHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interacting with NIMA and attenuating its mitosis-promoting activity. Displays a preference for an acidic residue N-terminal to the isomerized proline bond. Catalyzing pSer/Thr-Pro cis/trans isomerizations (By similarity).
MADERKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Essential PPIase that regulates mitosis presumably by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-JUL-2004 (Rel. 44, Last annotation update)
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5.2.1.8)
(Rotamase Pinl) (PPIase Pinl).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20070807; PubMed=10600477; DOI=10.1006/bbrc.1999.1736; Pujimori P., Takahashi K., Uchida C., Uchida T.; "Mice lacking Pinl develop normally, but are defective in entering cell cycle from GO arrest.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                121 DLGAPSRGQMQKPFEDASPALRTGEMSGPVFTDSGIHIILRTE 163
                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 265:658-663(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PIN1 MOUSE
Q9QUR7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Pin1;
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SO THE BREEF BREEF

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Attached 12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Attached R.L., Sthanear C.M., Schuler G.D., Attached S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Ropking R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., A Hopking R.P., Jordan H., Moore T., Rubin G.M., Hong L., Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rapleton M., Usdin T.B., Tochhyuki S., Carninci P., Prange C., Rab Erownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A., Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Glibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rakeeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rakieglez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arren M. A., Arren M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arren M. A., Arren M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arren M. A., Arren M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arren M. A., Arren M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arren M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arren M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arren M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arren M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arren M. A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rodriguez A.C., Grimwood J., Schmu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKARG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 LVKHNQSRRPSSWRQDKITRSKDEALELINGYIQKMKSGBEDFESLASQFSDCSSAKAGG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones 8.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MADEBKLPPGWEKRMSRSSGRVYYFNHMTNASQWERP----IAGGKNGQGEPGKVRCSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MADERKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                               GO; GO:0016853; F:1somerase activity; IEA.
GO; GO:0001755; F:1somerase activity; IEA.
GO; GO:0003755; F:peptidy1-proly1 cis-trans isomerase activity; IEA.
GO; GO:0006457; P:protein folding; IEA.
InterPro; IPR002297; Rotamase.
InterPro; IPR002202; WW.
Pfam; PR00439; Rotamase; I.
Pfam; PR00439; WWDMIN.
SMART; SM00456; WW; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                     -1- SIMILARITY: Belongs to the ppiC/parvulin rotamase family EMBL; AF239760; AAF43897.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DLGAFSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILRTE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 DLGSFGKGAMQKPFEDASFALRPGEMSGPVFTDSGIHIILRTE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 AA; 17671 MW; 4E54F66F16C9DF1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

88.4%; Score 753; DB 2;
Best Local Similarity 87.1%; Pred. No. 3.6e-61;
Matches 142; Conservative 11; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO1096; PPIC PPIASE 1; 1. PROSITE; PS50198; PPIC PPIASE 2; 1. PROSITE; PS01159; WW DOMAIN 1; 1. PROSITE; PS50020; WW DOMAIN 2; 1.
      Science 287:1644-1647(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isomerase; Rotamase.
SEQUENCE 159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
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      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HILVKHSQSRRPSSWRQEKITRSKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLLVKHSQSRRPSSWRQEKITRTKEBALELINGYIQKIKKGGEBDFESLASQPSDCSSAKA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MADEBKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGG--KNGQGEPARVRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20165035; PubMed=10698738; DOI=10.1126/science.287.5458.1644; Winkler K.E., Swenson K.I., Kornbluth S., Means A.R.; "Requirement of the prolyl isomerase Pinl for the replication
CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                    -!- SUBCELLUIAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the ppic/parvulin rotamase family.
-!- SIMILARITY: Contains 1 WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 RGDLGPPSRGQMQKPFBDASFALRTGEMSGPVFTDSGIHIILRTE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGDLGAFSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILRTE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0042127; P:regulation of cell proliferation; IMP. InterPro; IPR00297; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 AA; 18370 MW; 188E95F009176B1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01096; PPIC PPIASE 1; 1.
PROSITE; PS01096; PPIC PPIASE 2; 1.
PROSITE; PS01198; WH DÖMAIN 1; 1.
PROSITE; PS50020; WH DÖMAIN 2; 1.
Cell cycle; Isomerase; Nuclear protein; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 814; DB 1;
Pred. No. 9.4e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AB009691; BAA87037.1; -.
KMBL, AB009692; BAA87038.1; -.
EMBL, AK003169; BAB22743.1; -.
EMBL, AK002665; BAB22270.1; -.
PIR, JC7136; JC7136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
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Pfam; PF00397; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 95.2
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1346036; Pinl.
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
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Q919K6; **0919K6**

RESULT 3

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   REPRESENTATION OF THE STATE OF 
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PubMed=12477932, DOI=10.1073/pnas.242603899;
PubMed=12477932, DOI=10.1073/pnas.242603899;
Rausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,
Bromstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Morley N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.M., Gay L.J., Hulyk S.W.,
N. Haland D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,
Makealey R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Rezywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 LVKHNQSRRPSSWRQDRITRTKDEALEHINGYIQKIKSGDEDFESLASRPSDCSSAKAGG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVKHSQSRRPSSWRQEKITRTKERALELINGYIQKIKSGEEDFESLASQFSDCSSAKARG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Embryo;
MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
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                                                                                                                                                                                                                                                                                                                                                                         Query Match

88.3%; Score 752; DB 2; Length 159;
Best Local Similarity 87.1%; Pred. No. 4.4e-61;

Matches 142; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 DLGSFGRGAMQKPFEDASFALRPGEMSGPVFTDSGIHILLRTE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILRTE 163
                                                                                                                                                                  Klein S., Gerhard D.S.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC081312; AAH81312.1; -.
Hypothetical protein.
SEQUENCE 159 AA; 17793 MW; A17A9C6C0E0AB858 CRC64;
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Bypotheital protein.
Xenopus laevis (African clawed frog).
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NCBI_TaxID=8355;
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Best Local Similarity
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                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                        TISSUE=Embryo;
Klein S., Gerh
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61 LVKHSQSRRPSSWRQEKITRTKERALELINGYIQKIKSGEEDFESLASQFSDCSSAKARG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MADBEKL, PPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein (Fragment).

Kenopus laevis (African clawed frog).

Kenopus laevis (African Clawed frog).

Kenopus laevis (African Clawed frog).

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Kenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                      Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DLGAPSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILRTE 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Isomerase; Rotamase.
SEQUENCE 159 AA; 17641 MW; C8CF4AB70E316D3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OGAZRS
OGAZRS;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.1%; Score 751; DB 2;
86.5%; Pred. No. 5.4e-61;
tive 12; Mismatches 6;
                                                                                                                        Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lung;
PubMed=12477932; DOI=10.1073/pnag.242603899;
                                                                                                                                                                                                                  EMBL; BC077181; AAH77181.1; ...
GO; GO:0016653; P:18comerase activity; IEA.
InterPro; IPR001297; Rotamase.
InterPro; IPR001249; WW.
InterPro; IPR001202; WW Rsp5 WWP.
Pfam; PP00679; Rotamase; 1.
Pfam; PP0097; WW; 1.
Pfam; PP009403; WWDOMAIN.
SMART; SM00456; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01096; PPIC_PPIASE_1; 1.
PROSITE; PS50199; WW_DOMAIN_1, 1.
PROSITE; PS01159; WW_DOMAIN_2; 1.
PROSITE; PS50020; WW_DOMAIN_2; 1.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                 Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 VKHSQSRRPSSWRQEKITRTKERALELINGYIQKIKSGEEDFFSLASQFSDCSSAKARGD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ADEEKLPPGWEKRAGRSSGRVYYFNIMTNASQWERP----IAGGKNGQGEPGKVRCSHLL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ADEBKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRSUBERYe; STRAINSHING-LYDE; TISSUBERYe; TISSUBERYE; DOI=10.1073/pnas.242603899; MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                   Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-1- SIMILMRITY: Belongs to the ppiC/parvulin rotamase family.
EMBL; BC077447; AAH77447.1; -.
GO; GO:0016853; F:isomerase activity; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 158 AA; 17539 MW; EB94FF9F7650FFA1 CRC64; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 LGSFGKGAMQKPFEDASFALRPGEMSGPVFTDSGIHIILRTE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 LGAPSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILRTE 163
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:73206.
0RFNames=zgc:73206;
Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.8%; Score 748; DB 2
87.0%; Pred. No. 1e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Isomerase, Rotamase. NON TER
                                                                                                                                                                                                                                                                                                        InterPro; IPR0002349; WW. amase.
InterPro; IPR002349; WW. amase.
InterPro; IPR001202; WW. Rep5 WWP.
Pfam; PP00439; Rotamase; 1.
PRINTS; PR00403; WWDOMAIN.
SMART; SM0456; WW; 1.
PROSITE; PS01096; PPIC PPIASE 1; 1.
PROSITE; PS01159; WW DOMAIN 1; 1.
PROSITE; PS01159; WW DOMAIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                           SEQUENCE PROM N.A.
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06 PEX1
06 PEX1
06 PEX1
06 PEX1
07 05 - J
07 05 - J
07 05 - J
08 PEX2
08 PEX
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Höpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko.L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rebey J., Helton E., Ketteman M.W., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
"Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKARG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MADEEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (CCT-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
EMBL; BC059553; AAH59553.1; -- SZEIN; ZBB-GENB-040426-114; zgc:73206.
GO; GO:0015853; F:isomerase activity; IEA.
GO; GO:0013755; F:ppptidyl-prolyl cis-trans isomerase activity; IEA.
GO; GO:000457; P:protein folding; IEA.
InterPro; IPR002297; Rotamase.
InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PF00539; Rotamase; 1.
Pfam; PF00537; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCP13948 (Fragment).
Name-agCGSA6; ORFNames=ENSANGG0000011536;
Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.9%; Score 681; DB 2; Length 15 Best Local Similarity 79.0%; Pred. No. 1.4e-54; Matches 128; Conservative 17; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DLGAFSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILRT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 DLGLFGRGQMQKPFBDASFALKVGDMSGPVFTDSGVHIILRT 158
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SEQUENCE 159 AA; 17706 MW; 1A836D6259D8B718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01096; PPIC_PPIASE_1; 1.
PROSITE; PS01099; WPIC_PPIASE_2; 1.
PROSITE; PS010159; WW_DOMAIN_1; 1.
PROSITE; PSS0020; WW_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Wild-type, TISSUE=Bye;
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us-10-616-410-2.rup

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EMBL;
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60 LLVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKAR 119
                                                                                                                                                                                                                                                                                                                                                                                                     88 LILVKHNKSRRPSSWREENITRSKEEALEILESYRKKIQSNEATLQELAQRYSDCSSAKRG 147
                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                               31 MSDGQETVPEGWEKRISRSIGMIYYLNVYIKESQWDPPIAPAEPANTN---EPHEVQCAH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maleszka R., de Couet H.G., Miklos G.L.G.;
"Date transferability from model organisms to human beings: insights
"Date transferability from model organisms from the functional genomics of the flightless region of Drosophila.",
Proc. Natl. Acad. Sci. U.S.A. 95:3731-3736(1998).
                                                                                                                                                                                                                                                                                                                                        1 MAD-EEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSH
                                                                                              HSSP, Q13526; 1P8A.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
GO; GO:0006457; P:protein folding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Cregon-R; TISSUB=Larva, and Pupae; STRAIN=Oregon-R; TISSUB=Larva, and Pupae; MEDLINE=96133954; PubMed=8552658; DOI=10.1073/pnas.93.1.447; Maleszka R., Hanes S.D., Hackett R.L., de Couet H.G., Miklos G.L.G. "The Drosophila melanogaster dodo (dod) gene, conserved in humans, functionally interchangeable with the ESS1 cell division gene of
         Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ppic/parvulin rotemase family.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL: AAAB01008898; EAA09299:1;--
                                                                                                                                                                                                                                                                                                                 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dodo protein.
Name-dodo ORFNames-CG17051;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Endopterygota; Diptera; Brithropoda; Brachycera; Muscomorpha; Rphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98188272; PubMed-9520435; DOI-10.1073/pnas.95.7.3731;
                                                                                                                                                                                                                                                                                     57.6%; Score 491; DB 2; Length 191; 58.0%; Pred. No. 58-37; ive 25; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          120 GDLGAFSRGQMQKPFBDASFALRTGEMSGPVFTDSGIHIILR 161
                                                                                                                                                                                                                                                              SEQUENCE 191 AA; 21872 MW; 7BD43BA02B0AD4B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 GDLGMFKRGMMQKPFEDAAFALKVGDMSDIVDTDSGVHLILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 93:447-451(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P54355; O61344; Q9VRH1;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
                                                                                                                                                                                              PROGITE; PSS0198; PPIC PPIASE 2; 1. PROSITE; PS01159; WW DOMAIN 1; 1. PROSITE; PS50020; WW DOMAIN 2; 1.
                                                                                                                                               Interpro; IPR00029;; Rotamase.
Interpro; IPR001202; WW Rsp5 WWP.
Pfam; PP00639; Rotamase; 1.
Pfam; PP00397; WW; 1.
                                                                                                                                                                                                                                                                                                                94; Conservative
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                                                                                                                                                                                                                                     Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                   Local Similarity
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SEQUENCE FROM N.A.
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STRAIN-PEST
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RA Adams M.D., Celniker S.E., 161 F.N., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., 161 F.N., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., 161 F.N., Fvans C.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Chango M., Richieffer B.D.,
RA Ballew R.M., Bax, A.M. H.-J., Andrewe-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Eusam D.A., Butler H., Cadleu B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Burtis K.C., Eusam D.A., Butler H., Cadleu B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J. H., Galleu B., Burtis M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Cadbriellan A.B., Gary R.S., Galbart W.M., Gabriellan A.B.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Reiner M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Reit V., Mattei B., McIntosh T.C., McLeod M.P., Davi V., Rese M.G.,
Ra Alazacolo M., Pitenan G.S., Pan S., Pollard J., Wang X.,
Shue B.C., Span-Himson J., Simpson M., Strong R., Wallenberden J.,
Rainer K., Tector C., Turner R., Venter E., Wang K., Wallenberden J., Wallenberden J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYMIL outstation the burpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeablesh.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426669; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield R.J., Bayraktaroglu L., Berman B.P., Betrencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!-SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
-!-SIMILARITY: Contains 1 WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PlyBase, FBGN0015379; dod.
InterPro, IPR000297; Rotamase.
InterPro, IPR001202; WW_R8p5_WWP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF017777; AAC28408.1; -. AE003568; AAF50829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U35140; AAC46958.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENOME REANNOTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ntAct; P54353;
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3 DNSLPAGWEKRQSR&NDRVYYFNTATGRSQWERP--DESAFGKG--SELKSVQCLHLLVK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 BEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSHLLVK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.2%; Score 436; DB 2; Length 168;
54.8%; Pred. No. 4.8e-32;
ive 17; Mismatches 45; Indels 14; Gaps

    SIMILARITY: Belongs to the ppiC/parvulin rotamase family.

                                                               Waterston R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SBP-2004) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS50198; WW; DPIC, PPICSE 2; 1.
PROSITE; PS50159; WW DOMAIN 1; 1.
PROSITE; PS50020; WW DOMAIN 2; 1.
PROSITE; PS50020; WW DOMAIN 2; 1.
SRQUENCE 168 AA; 19176 MW; 0PC837780579C070 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wormbase; WBGene00022448; Y110A2AL.13.
Wormbep; Y110AAZ.1.3; CB25189.
GO; GO:001683; F'isomerase activity; IEA.
InterPro; IPR000297; Rocamase.
InterPro; IPR001202; WW Rsp5_WWP.
PF00639; Rocamase; 1.
Pfons, PF00639; WW; 1.
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                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
Submitted (OCT-2002)
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Submitted (NOV-2002)
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Submitted (JUN-2002)
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Submitted (FEB-2003)
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Submitted (MAR-2003)
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Submitted (MAY-2003)
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WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                 TRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A. STRAIN-Bristol N2;
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         SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LHLLVKHKGSRRPSSWREANITRTKEEAQLLLEVYRNKIVQQRATFDELARSYSDCSSAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MPDAROLPDGWEKRISRSTGMSYYLNMYTKESQWDQPTEPAKKAGGGSAGGDAPDEVHC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MADEEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPS--GNSSSGGKNGQGE-PARVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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"Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                      Match 53.6%; Score 456.5; DB 1; Length 166; Local Similarity 56.7%; Pred. No. 6.2e-34; Los 93; Conservative 16; Mismatches 52; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 ARGDIGAFSRGOMOKPFEDASFALRIGEMSGPVFTDSGIHIILR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R_{.,i} Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. [6]
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                     44 44 A A -> T (in Ref. 2).
166 AA; 18376 MW; 3B4306FA930E7259 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein Y110A2AL.13.
Name=Y110A2AL.13; ORFNames=Y110A2AL.13;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -OCT-2000 (TrEMBLrel. 15, Created)
                                                   SMART; SM00456; WW; 1.
PROSITE; PS01096; PPIC PPIASE 1; 1.
PROSITE; PS50196; PPIC PPIASE 2; 1.
PROSITE; PS501159; WW DOMAIN 1; 1.
PROSITE; PS50020; WW DOMAIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99069613; PubMed=9851916;
Pfam; PF00639; Rotamase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                       Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NormBase Consortium
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                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09N492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 ETGLPEDWEVRHSOSKNLPYYFNSATKTSRWEPPSGTDVDKLKIYMAKYHSPTSQQQQQQ 65
                         104 ESLASQFSDCSSAKARGDLGAFSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein folding.";
J. Blol. Chem. 273:31971-31976(1998).

-!- FUNCTION: Site-specific PPrase with respect to the amino acid N-terminal to the proline residue. Peptides with glutamate, phosphoserine, or phosphothreconine in the -1 position are the best substrates. It is not only able to isomerize small peptides but is also active in protein folding.
-!- CATALITIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 ASQFSDCSSAKARGDLGAFSRGÖMQKPFEDASFALRTGEMSGPVPTDSGIHIILRTE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Gaps
                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Peptidyl-prolyl cis-trans isomerase sspl (RC 5.2.1.8) (PPlase sspl).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site specific parvulin homolog from N. crassa active in
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=99041963; PubMed=9822668; DOI=10.1074/jbc.273.48.31971;
                                                                                                                                                                                                                                                                                                                                                          Sordariomycetes;
Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kops O., Eckerskorn C., Hottenrott S., Fischer G., Mi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC8D0497DFFF7339 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 EEKL.PPGWEKRMSRSSGRVYYFNHITNASQWERPSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.3%; Score 428.5; DB 1;
50.8%; Pred. No. 2.6e-31;
ive 20; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Fungi, Ascomycota, Pezizomycotina,
Sordariomycetidae, Sordariales, Sordariaceae,
                                                                                                                                                                182 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gln-rich.
PpiC.
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50198; PPIC_PPIASE_2; 1. PROSITE; PS01159; WW DOWAIN 1; 1. PROSITE; PS50020; WW_DOWAIN_2; 1. Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, Q13526; 1F8A.
InterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW RspS_WWP.
Pfam; PF00639; Rotamase; 1.
Pfam; PF00639; WW; 1.
SWART; SM00456; WW; 1.
                                                                                                                                                                                                             (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ006023; CAA06818.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 AA; 20673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.8 Matches 90; Conservative
                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                        Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fropschug M.;
                                                                                                                                                                                                             10-OCT-2003
                                                                                                                                                                                                                                                                                                             Name=88p-1;
                                                                                                                                                              SSP1 NEUCR
060045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                          SSP1_NEUCR
                                        셤
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ò
                      HSQSRRPSSWRQEKITRTKERALELING-----YIQKIKSG---EEDFESLASQFSDC 113
                                               HDGSRNPSSWRSDHITRSKDDAINILKSADLRNFHYEKELKDASNIEGKFFRELAKOFSDC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 GKNGQGEP-ARVRCSHILVKHSQSRRPSSWRQBKITRTKERALELINGYIQKIKSGEEDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QQQQQQQQGKIRCAHLLVKHNQSRRPSSWRBSEITRTKQBALTTLQGFBQRIKSGSISL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
A Elkine T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
A Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
Roy A., Poley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
Ramal M., Kamysselis M., Maucell E., Bielke C., Rudd S., Frishman D.,
Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
DeSouza C. C., Glass L., Orbech M.J., Berglund J., Voelker R.,
Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
The Genome Sequence of the Filamentous Pungus Neurospora crassa.";
Nature Oi-O(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MADBEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSG-------NSSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016853; F:1somerase activity; IEA.
GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
GO; GO:0006457; P:protein folding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora crassa.
Bukaryota, Pungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.9%; Score 433.5; DB 2; Length 186; 51.1%; Pred. No. 9.2e-32;
                                                                                                                   SSAKARGDLGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHILLR 161
                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (AJ006023) peptidylprolyl isomerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 AA; 21175 MW; B8E214B1E01AEA36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50198; PPIC PPIASE_2; 1.
PROSITE; PS61159; WW DOMALN 1; 1.
PROSITE; PS50020; WW DOMALN 2; 1.
Hypothetical protein; Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR000297; Rotamase.
Interpro; IPR001202; WW_Rsp5_WWP.
                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 26, (TrEMBLrel. 26, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00639; Rotamase; 1.
Pfam; PF00397; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91, Conservative
                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.
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Matches 91: Common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=OR74A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=NCU08554.1
                                                                                                                                                                                                                                                                                                                                   01-MAR-2004
                                                                   29
                                                                                                                   114
                      64
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MEDLINE=21648401; PubMed=11859360; DOI=10.1038/narure724;
Mod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
By Squure J., Peat N., Hayles J., Basker S., Baskam D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraeer A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huche E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quali M.A., Rabbinowitsch B.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Moodward J., Volckaert G., Aert R., Roben J., Grymonprez B.,
Weltjens I., Vanstreels B., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritzc C., Holzer B., Moestl D., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 -RVRCSHLLVKHSOSRRPSSWRQEKITRTKBEALELINGYIQKIKSGEEDFESLASQFSD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 GKIRCSHLLVKHRDSRRPSSWREAEITRTKEEARBILRGHGERIWRGEIRLGDLAMSESD 125
                          MEDLINE=98151356; PubMed=9482729; DOI=10.1093/emboj/17.5.1315;
Crenablaw D.G., Yang J., Means A.R., Kornbluth S.;
"The mitotic peptidyl-prolyl isomerase, Pinl, interacts with Cdc25 and Plx1.";
EMBO J. 17.1315-1327(1998).
-i- SHNLIARITY: Belongs to the ppiC/parvulin rotamase family.
EMBL; AF035768; AAC49984.1; -.
HSSP; Q13526; IPPA.
GO; GO:0016853; F:seomerase activity; IEA.
GO; GO:0016853; F:sprotein Folding; IEA.
GO; GO:0003755; F:sprotein Folding; IEA.
InterPro; IPR001202; WW Rap5_WWP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNS------SSGGKNGQGEPA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LPAGWEVRHSNSKNLPYYPNPATRESRWEPPADTDMETLKMYMATYHSGAATYHEAPSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 CSSAKARGDLGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILRTE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 AA; 20038 MW; 1D1E8376239E1309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-GCT-2004 (Rel. 45, Last annotation update)
Peptidyl-prolyl cis-trans isomerase pinl (RC 5.2.1.8).
Name-pinl, ORFNames-SPCCI6C4.03,
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Pungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae, Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.6%; Score 397; DB 2;
48.0%; Pred. No. 1.9e-28;
iive 24; Mismatches 51;
                                                                                                                                                                                                                                                                                                                     Pfam; PP00639; Roteamase; 1.
Pfam; PP00397; WW; 1.
SNART; SMO0456; WW; 1.
PROSITE; PS50199; PPIC PPIASE 2; 1.
PROSITE; PS50129; WW DÖMAIN 1; 1.
PROSITE; PS50020; WW DOMAIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase; Rotamase. SEQUENCE 176 AA;
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074448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
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126 ALTESDCSSARKRGDLGYFGRGDMQKEFEDAAFALKPGEISDIVDTASGLHLIERLE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ETGLPSGWEVRHSNSKNLPYYPNPITKESRWEPPSNTDTEKLKEYMAQHHSGLAERNNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SSGGKNGQGEPARVRCSHLLVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
EMBL, AY374446; AAQ83700.1; -.
GO; GO:0016853; F:lsomerase activity; IRA.
GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IRA.
GO; GO:0006457; P:protein folding; IRA.
InterPro; IPR010297; Rotamase.
InterPro; IPR010297; WW R8PS_WWR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Domingos P.C., Pereira M., Castro N.S., Felipe M.S.S., Soares C.M.A.
Jesuino R.S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                  Bukaryota, Pungi, Ascomycota, Pezizomycotina, Burotiomycetes,
Onygenales, mitosporic Onygenales, Paracoccidioides.
NCBI_TaxID=121759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.9%; Score 408.5; DB 2; Length 190; 44.9%; Pred. No. 1.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 AA; 20983 MW; 710DCBEFAA9238AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 EEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNS----
                                                                                                                                                                               05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 44.9%; Pred. No. 1.9e-
hes 83; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emericella nidulans (Aspergillus nidulans).
                                                                                                                                                                                                                                                         Peptidyl-prolyl cis/trans isomerase. Paracoccidioides brasiliensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptidyl-prolyl cis/trans isomerase.
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Pfam; PP00397; WW; 1.
SMART; SM0645; WW; 1.
PROSITE; PS50198; PP1C PPIASE 2; 1.
PROSITE; PS01159; WW DOWAIN 1; 1.
PROSITE; PS50020; WW DOWAIN 2; 1.
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                Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B., Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G Daga R.R., Curzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
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                                                                                                                                                                                                                             FUNCTION, AND SUBCELLULAR LOCATION.
MEDLINE=21564328; PubMed=11707530;
Huang H.-K., Forsburg S.L., John U.P., O'Connell M.J., Hunter T.;
"Isolation and characterization of the Pinl/Essip homologue in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 CSSARRGGELGEFGRDEMQKPFEDAAPALKPGEISGVVETSSGFHIIQR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSSAKARGDLGAPSRGOMOKPFEDASFALRTGEMSGPVPTDSGIHIILR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.6%; Score 388.5; DB 1; Length 175; 48.5%; Pred. No. 1.1e-27; tive 21; Mismatches 51; Indels 15.
                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLUIAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
-!- SIMILARITY: Contains 1 WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 175 PpiC.
175 AA; 19773 MW; ABA637835471BD25 CRC64;
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nterPro, IPR000297; Rotamase.
nterPro, IPR001202; WW_R8p5_WWP
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PIR; T41093; T41093.
                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe."
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fam; PF00397; WW; 1.
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nes 82; Conservative
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